

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Wolf, Marcia K
Cassels, Fred J
Boedeker, Edgar C
- (ii) TITLE OF INVENTION: Transformed Bacteria Producing GS6
Antigens as Vaccines
- (iii) NUMBER OF SEQUENCES: 10
- (iv) CORRESPONDENCE ADDRESS:
 - (A) ADDRESSEE: Hendricks and Assoc
 - (B) STREET: P.O. Box 2509
 - (C) CITY: Fairfax
 - (D) STATE: VA
 - (E) COUNTRY: US
 - (F) ZIP: 22031
- (v) COMPUTER READABLE FORM:
 - (A) MEDIUM TYPE: Floppy disk
 - (B) COMPUTER: IBM PC compatible
 - (C) OPERATING SYSTEM: PC-DOS/MS-DOS
 - (D) SOFTWARE: PatentIn Release #1.0, Version #1.25
- (vi) CURRENT APPLICATION DATA:
 - (A) APPLICATION NUMBER: US 09/479,877
 - (B) FILING DATE: 10-JAN-2000
 - (C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:
 - (A) NAME: Hendricks, Glenna M
 - (B) REGISTRATION NUMBER: 32,535
- (ix) TELECOMMUNICATION INFORMATION:
 - (A) TELEPHONE: 703/425-8405
 - (B) TELEFAX: 703/425-8406

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 4875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: DNA (genomic)
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

AAGCTTGATA	CCAGTTGATA	AAAATATATC	ACGCTGGAA	TGACGTGATG	TATATACGGA	60
GCAGCTATGT	CGGAACAGAT	ATTTTCCTAT	CGGTATGCGT	TGTGAGTAAG	CGTAAAGCCA	120
ATGCTGTCTG	TAACTCCTGA	TCCTTGCAGA	CTAAATTAGA	GCTCCTTCTA	AATTAGACGG	180
ATGGATAAAC	CTACAGACTG	GCGCTCTGGG	TCTCGCCGGA	TATTTCTAA	TGAATTAAAG	240
CTTCATATGG	TTGAACTGGC	TTCGAAACCA	AATGCCAATG	TCGCACAACT	GGCTCGGGAA	300
CATGGCGTTG	ATAACAACCT	GATTTTAAA	TAGCTACGCC	TCTGGCAAAG	AGAAGGACGT	360
ATTTCTCGTA	GAATGCCTCC	AACTATTGTA	GGCCCTACAG	TACCACTGAG	GTAGCCTGAA	420
TTTAAAGCCG	AAGCGGTCAG	AACTGTTCTT	GGTGTGAACG	TAGCACTCAC	CAATAAAAGC	480
ATCAATACGG	TGCTCTGTTG	ACACATTACG	AATGTTATGT	ATACAATAAA	AATGATTATA	540
GCAATATTAA	TGGTGTATA	TGAAGAAAAC	AATTGGTTA	ATTCTAATTTC	TTGCTTCATT	600
CGGCAGCCAT	GCCAGAACAG	AAATAGCGAC	TAAAAACTTC	CCAGTATCAA	CGACTATTC	660
AAAAAGTTT	TTTGCACCTG	AACCACGAAT	ACAGCCTCT	TTTGGTGAAA	ATGTTGGAAA	720
GGAAGGAGCT	TTATTATTTA	GTGTGAACCT	AACTGTTCT	GAAAATGTAT	CCCAGGTAAC	780
GGTCTACCCCT	GTTCATGATG	AAGATTATGG	GTTAGGACGA	CTAGTAAATA	CCGCTGATGC	840
TTCCAATCA	ATAATCTACC	AGATTGTTGA	TGAGAAAGGG	AAAAAAATGT	TAAAAGATCA	900
TGGTGCAGAG	GTTACACCTA	ATCAACAAAT	AACTTTAAA	GCGCTGAATT	ATACTAGCGG	960
GGAAAAAAAAA	ATATCTCCTG	GAATATATAA	CGATCAGGTT	ATGGTTGGTT	ACTATGTAAA	1020
CTAAATACTG	GAAGTATGAT	TATGTTGAAA	AAAATTATTT	CGGCTATTGC	ATTAATTGCA	1080
GGAACTTCCG	GAGTGGTAAA	TGCAGGAAAC	TGGCAATATA	AATCTCTGGA	TGTAAATGTA	1140
AATATTGAGC	AAAATTATTT	TCCAGATATT	GATTCCGCTG	TTCGTATAAT	ACCTGTTAAT	1200
TACGATTCGG	ACCCGAAACT	GGATTCACAG	TTATATACGG	TTGAGATGAC	GATCCCTGCA	1260
GGTGTAAAGCG	CAGTTAAAAT	CGCACCAACA	GATAGTCTGA	CATCTTCTGG	ACAGCAGATC	1320
GGAAAGCTGG	TTAATGTAAA	CAATCCAGAT	CAAATATGA	ATTATTATAT	CAGAAAGGAT	1380
TCTGGCGCTG	GTAACTTAT	GGCAGGACAA	AAAGGATCCT	TTCCGTCAA	AGAGAATACG	1440
TCATACACAT	TCTCAGCAAT	TTATACTGGT	GGCGAATACC	CTAATAGCGG	ATATTGCTCT	1500

GGTACTTATG CAGGAAATT GACTGTATCA TTTACAGCA ATTAAAAAAA GGCCGCATTA	1560
TTGCGGCCAT TGACGATACT GCTAGGCAAA AATATGAAAT CAAAGTTAAT TATACTATTG	1620
ACGTTAGTGC CATTTCATC TTTTCAACA GGAAATAATT TTGAAATAAA TAAGACACGA	1680
GTAATTTACT CTGACAGCAC ACCATCAGTT CAAATATCAA ATAATAAAGC ATATCCTTA	1740
ATTATTCAAA GCAATGTATG GGATGAAAGC AATAATAAAA ATCATGACTT TATAGCAACA	1800
CCACCGATTT TTAAAATGGA AAGTGAAAGT CGGAATATAA TAAAATAAT TAAAACAAC	1860
ATTAATTGCG CGGACTCTCA GGAAAGTATG AGATGGTTAT GTATTGAATC AATGCCACCA	1920
ATAGAAAAAA GTACTAAAAT AACAGAAAA GAAGGAAGGA CAGACAGTAT TAATATCAGC	1980
ATTCGGGGGT GCATTAAACT GATATATCGA CCTGCCAGTG TTCCGTCTCC TGTTTTAAT	2040
AATATAGTAG AAAAATTAAA ATGGCATAAA AATGGAAAGT ATCTTGTATT AAAAATAAT	2100
ACACCCTATT ACATTAGCTT TTCTGAGGTT TTTTGATT CAGATAAAGT AAACAATGCA	2160
AAAGATATTT TATATGTAAA ACCATACTCA GAGAAGAAAA TAGATATCAG CAACAGAATA	2220
ATAAAAAAA TCAAATGGGC TATGATTGAT GATGCTGGCG CAAAAACAAA ACTTTATGAA	2280
TCAATTATAT AAAAATCTC ATTACAGTAT ACAAAACAT CAGATTACAG GCTTGCTTT	2340
TTTGCTATTT ATATATCCTT TCTAACCTC ATATGGAAAT GAACAATTAA GTTTGACTC	2400
ACGATTCCCTA CCATCAGGTT ATAATTACTC TTTAAATAGT AACTTACCTC CTGAAGGTGA	2460
GTATCTGGTT GATATTTATA TTAACAAAAT AAAAAGGAG TCCGCGATTA TTCCTTTTA	2520
TATAAAAGGA AATAAACTTG TACCATGTTT ATCAAAAGAA AAAATTCAT CTTTGGGTAT	2580
CAACATTAAT AATAACGACA ACACAGAGTG TGTAGAAACA AGTAAGGCAG GTATTAGTAA	2640
TATCAGCTTT GAGTTTAGCT CTCTCGTTT GTTTATTGCT GTACCGAAAA ATCTTCTGTC	2700
TGAGATTGAT AAAATATCAT CAAAGGATAT AGATAACGGG ATTCAATGCTT TATTTTTAA	2760
TTATCAAGTA AATACAAGGC TAGCCAATAA TAAAATCGT TATGATTACA TTTCTGTTTC	2820
ACCAAATATA AATTATTTT CATGGCGGTT GCGTAATCTT TTTGAATTAA ACCAAAACAA	2880
CGATGAAAAA ACATGGAAA GAAACTACAC TTATCTAGAA AAAAGTTTT ATGATAAAAA	2940
GCTAAACTTA GTCGTTGGTG AAAGTTATAC GAATTCAAAT GTTTATAATA ACTACTCTT	3000
TACTGGTATT TCAGTTCTA CAGATACAGA TATGTATACG CCAAGTGAAA TCGATTATAC	3060
ACCAGAAATT CATGGAGTGG CTGATTCAAGA CTCTCAGATT ATTGTCAGGC AAGGCAACAC	3120

CATTATCATT AATGAAAGTG TTCCAGCCGG ACCGTTCTCA TTTCCAATAA CCAATCTCAT	3180
GTATACTGGG GGGCAACTTA ATGTGGAGAT AACAGATATT TATGGAAATA AAAAACAAATA	3240
TACTGTCAAT AATTCCCTCTC TTCCTGTTAT GAGAAAAGCG GGACTAATGG TATATAATTT	3300
TATATCTGGG AAATTAACAA AAAAAAATAG TGAGGGATGGT GATTTTTTA CTCAAGGTGA	3360
TATTAACACT GGTACTCACT ATAACAGCAC ACTATTGGT GGATATCAGT TTAGTAAAAA	3420
TTATTTAAC TTATCTACTG GTATAGGCAC TGATCTGGGA TTTCTGGAG CATGGCTACT	3480
ACACGTTAGC AGAAGTAATT TTAAGAATAA AAATGGATAT AATATTAATC TACAACAAAA	3540
CACTCAGTTA AGACCATTCA ATGCCGGGGT TAATTCGAT TACGCATACA GAAAAAAAAG	3600
GTATGTGGAA CTTTCCGACA TTGGCTGGCA TGGTAATTAA TATAATCAAC TTAAAAATAG	3660
TTTTCTTTA TCCTTGTCAA AATCATTGAA TAAATACGGA AATTCTCAC TTGATTATAA	3720
CAAAATGAAA TACTGGGATA ATGCGTATGA TAGTAACTCA ATGTCGATTC GTTATTTTT	3780
TAAATTCAATG CGAGCAATGA TTACAACAAA TTGTTCTTTA AATAAATATC AATCTTATGA	3840
AAAAAAAGAT AAAAGATTAA GTATTAATAT ATCATTGCCT TTAACCAAAG ATTACGGGCA	3900
CATATCTTCA AACTATTCAAT TTTCCAATGC AAATACAGGA ACGGCAACCA GTTCTGTAGG	3960
CTTAAACGGT AGTTTTTTA ATGACGCAAG ATTAAACTGG AACATTCAAG AGAACAGAAC	4020
GACCCGTAAC AATGGATATA CTGATAATAC CAGTTACATA GCAACCAGCT ATGCCTCTCC	4080
CTATGGCGTT TTTACTGGTT CATATTCAAGG ATCGAACAAAG TATTCAAGCC AGTTTTATTC	4140
TGCATCGGGGA GGTATTGTT TGCATAGCGA TGGCGTAGCT TTTACTCAAA AAGCCGGAGA	4200
TACCTCTGCT CTTGTCCGTA TTGATAATAT TTCTGATATA AAAATTGGTA ACACCTCTGG	4260
TGTTTATACT GGGTATAATG GTTTGCTTT AATTCCAT CTTCAGCCGT TCAAAAAAAA	4320
CACCATTAAATTA ATTAATGATA AAGGAATTCC AGACGGTATT ACTCTTGCTA ATATAAAAAAA	4380
ACAAGTTATC CCATCACGAG GAGCTATTGT TAAAGTAAAA TTTGATGCTA AAAAAGGCAA	4440
TGACATTTG TTTAAGCTTA CAACTAAAGA TGGAAAAACG CCCCCATTAG GAGCTATAGC	4500
CCATGAAAAA AATGGAAAAC AGATTAATAC GGGTATCGTT GACGATGATG GTATGCTTTA	4560
TATGTCTGGA TTATCAGGGAA CAGGGATTAT TAATGTAACA TGGAATGGAA AAGTCTGTTC	4620
ATTTCTTTT TCAGAAAAAG ATATATCTAG CAAACAATTA TCTGTTGTAA ATAAACAATG	4680
TTAGGTAGTG CATCCAATTAA GTAGAACATG TGTTTTCGA TAAACGCTCC GATCTTTT	4740

TCGTGGATCT CAACTGAGCG TGAGAAGCAG ATTGTTTAC GAGCCAACCG CTTAATGCGG 4800
GTGCGTAGCG TCAGATTATT ACGCTCAATG CGTTGGGTGA ATATTTGCC GGTCAGATGC 4860
TTATTCTTCG GTACC 4875

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 18 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GGCCGCATTA TTGCGGCC

18

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 22 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

GGCCGCATTA TTGATTGCGG CC

22

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 527 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: DNA (genomic)

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

TTGACACATT ACGAATGTTA TGTATAACAAT AAAAATGATT ATAGCAATAT TAATGGTGT	60
ATATGAAGAA ACAATTGGT TTAATTCTAA TTCTTGCTTC ATTCCGCAGC CATGCCAGAA	120
CAGAAATAGC GACTAAAAAC TTCCCAGTAT CAACGACTAT TTCAAAAAGT TTTTTGCAC	180
CTGAACCACG AATACAGCCT TCTTTGGTG AAAATGTTGG AAAGGAAGGA GCTTTATTAT	240
TTAGTGTGAA CTTAACTGTT CCTGAAAATG TATCCCAGGT AACGGTCTAC CCTGTTTATG	300
ATGAAGATTA TGGGTTAGGA CGACTAGTAA ATACCGCTGA TGCTTCCCAA TCAATAATCT	360
ACCAGATTGT TGATGAGAAA GGGAAAAAAA TGTTAAAAGA TCATGGTGCA GAGGTTACAC	420
CTAATCAACA AATAACTTT AAAGCGCTGA ATTATACTAG CGGGGAAAAAA AAAATATCTC	480
CTGGAATATA TAACGATCAG GTTATGGTTG GTTACTATGT AAACTAA	527

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 154 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Lys Thr Ile Gly Leu Ile Leu Ile Leu Ala Ser Phe Gly Ser			
1	5	10	15

His Ala Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr			
20	25	30	

Ile Ser Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe			
35	40	45	

Gly Glu Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu			
50	55	60	

Thr Val Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp
65 70 75 80

Glu Asp Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln
85 90 95

Ser Ile Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys
100 105 110

Asp His Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala
115 120 125

Leu Asn Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn
130 135 140

Asp Gln Val Met Val Gly Tyr Tyr Val Asn
145 150

(2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 167 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Leu Lys Lys Ile Ile Ser Ala Ile Ala Leu Ile Ala Gly Thr Ser
1 5 10 15

Gly Val Val Asn Ala Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn
20 25 30

Val Asn Ile Glu Gln Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg
35 40 45

Ile Ile Pro Val Asn Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu
50 55 60

Tyr Thr Val Glu Met Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile
65 70 75 80

Ala Pro Thr Asp Ser Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu
85 90 95

Val Asn Val Asn Asn Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys
100 105 110

Asp Ser Gly Ala Gly Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro
115 120 125

Val Lys Glu Asn Thr Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly
130 135 140

Glu Tyr Pro Asn Ser Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu
145 150 155 160

Thr Val Ser Phe Tyr Ser Asn
165

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Asn Asn Phe Glu Ile Asn Lys Thr Arg Val Ile Tyr Ser Asp Ser Thr
1 5 10 15

Pro Ser Val Gln Ile Ser Asn Asn Lys Ala Tyr Pro Leu Ile Ile Gln
20 25 30

Ser Asn Val Trp Asp Glu Ser Asn Asn Lys Asn His Asp Phe Ile Ala
35 40 45

Thr	Pro	Pro	Ile	Phe	Lys	Met	Glu	Ser	Glu	Ser	Arg	Asn	Ile	Ile	Lys
50						55						60			
Ile Ile Lys Thr Thr Ile Asn Leu Pro Asp Ser Gln Glu Ser Met Arg															
65					70				75			80			
Trp Leu Cys Ile Glu Ser Met Pro Pro Ile Glu Lys Ser Thr Lys Ile															
85				88			90					95			
Asn Arg Lys Glu Gly Arg Thr Asp Ser Ile Asn Ile Ser Ile Arg Gly															
100					105						110				
Cys Ile Lys Leu Ile Tyr Arg Pro Ala Ser Val Pro Ser Pro Val Phe															
115				118		120					125				
Asn Asn Ile Val Glu Lys Leu Lys Trp His Lys Asn Gly Lys Tyr Leu															
130					135					140					
Val Leu Lys Asn Asn Thr Pro Tyr Tyr Ile Ser Phe Ser Glu Val Phe															
145				148		150			155			160			
Phe Asp Ser Asp Lys Val Asn Asn Ala Lys Asp Ile Leu Tyr Val Lys															
165				168		170			175						
Pro Tyr Ser Glu Lys Lys Ile Asp Ile Ser Asn Arg Ile Ile Lys Lys															
180				183		185				190					
Ile Lys Trp Ala Met Ile Asp Asp Ala Gly Ala Lys Thr Lys Leu Tyr															
195				198		200				205					
Glu Ser Ile Leu															
210															

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 802 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: unknown
- (ii) MOLECULE TYPE: peptide
- (iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met Asn Gln Phe Tyr Lys Lys Ser His Tyr Ser Ile Gln Lys His Gln
1 5 10 15

Ile Thr Gly Leu Leu Phe Leu Leu Phe Ile Tyr Pro Phe Ser Thr Ser
20 25 30

Tyr Gly Asn Glu Gln Phe Ser Phe Asp Ser Arg Phe Leu Pro Ser Gly
35 40 45

Tyr Asn Tyr Ser Leu Asn Ser Asn Leu Pro Pro Glu Gly Glu Tyr Leu
50 55 60

Val Asp Ile Tyr Ile Asn Lys Ile Lys Lys Glu Ser Ala Ile Ile Pro
65 70 75 80

Phe Tyr Ile Lys Gly Asn Lys Leu Val Pro Cys Leu Ser Lys Glu Lys
85 90 95

Ile Ser Ser Leu Gly Ile Asn Ile Asn Asn Asn Asp Asn Thr Glu Cys
100 105 110

Val Glu Thr Ser Lys Ala Gly Ile Ser Asn Ile Ser Phe Glu Phe Ser
115 120 125

Ser Leu Arg Leu Phe Ile Ala Val Pro Lys Asn Leu Leu Ser Glu Ile
130 135 140

Asp Lys Ile Ser Ser Lys Asp Ile Asp Asn Gly Ile His Ala Leu Phe
145 150 155 160

Phe Asn Tyr Gln Val Asn Thr Arg Leu Ala Asn Asn Lys Asn Arg Tyr
165 170 175

Asp Tyr Ile Ser Val Ser Pro Asn Ile Asn Tyr Phe Ser Trp Arg Leu
180 185 190

Arg Asn Leu Phe Glu Phe Asn Gln Asn Asn Asp Glu Lys Thr Trp Glu
195 200 205

Arg Asn Tyr Thr Tyr Leu Glu Lys Ser Phe Tyr Asp Lys Lys Leu Asn
210 215 220

Leu Val Val Gly Glu Ser Tyr Thr Asn Ser Asn Val Tyr Asn Asn Tyr
225 230 235 240

Ser Phe Thr Gly Ile Ser Val Ser Thr Asp Thr Asp Met Tyr Thr Pro
245 250 255

Ser Glu Ile Asp Tyr Thr Pro Glu Ile His Gly Val Ala Asp Ser Asp
260 265 270

Ser Gln Ile Ile Val Arg Gln Gly Asn Thr Ile Ile Ile Asn Glu Ser
275 280 285

Val Pro Ala Gly Pro Phe Ser Phe Pro Ile Thr Asn Leu Met Tyr Thr
290 295 300

Gly Gly Gln Leu Asn Val Glu Ile Thr Asp Ile Tyr Gly Asn Lys Lys
305 310 315 320

Gln Tyr Thr Val Asn Asn Ser Ser Leu Pro Val Met Arg Lys Ala Gly
325 330 335

Leu Met Val Tyr Asn Phe Ile Ser Gly Lys Leu Thr Lys Lys Asn Ser
340 345 350

Glu Asp Gly Asp Phe Phe Thr Gln Gly Asp Ile Asn Tyr Gly Thr His
355 360 365

Tyr Asn Ser Thr Leu Phe Gly Gly Tyr Gln Phe Ser Lys Asn Tyr Phe
370 375 380

Asn Leu Ser Thr Gly Ile Gly Thr Asp Leu Gly Phe Ser Gly Ala Trp
385 390 395 400

Leu Leu His Val Ser Arg Ser Asn Phe Lys Asn Lys Asn Gly Tyr Asn
405 410 415

Ile Asn Leu Gln Gln Asn Thr Gln Leu Arg Pro Phe Asn Ala Gly Val
420 425 430

Asn Phe Asp Tyr Ala Tyr Arg Lys Lys Arg Tyr Val Glu Leu Ser Asp
435 440 445

Ile Gly Trp His Gly Asn Leu Tyr Asn Gln Leu Lys Asn Ser Phe Ser
450 455 460

Leu Ser Leu Ser Lys Ser Leu Asn Lys Tyr Gly Asn Phe Ser Leu Asp
465 470 475 480

Tyr Asn Lys Met Lys Tyr Trp Asp Asn Ala Tyr Asp Ser Asn Ser Met
485 490 495

Ser Ile Arg Tyr Phe Phe Lys Phe Met Arg Ala Met Ile Thr Thr Asn
500 505 510

Cys Ser Leu Asn Lys Tyr Gln Ser Tyr Glu Lys Lys Asp Lys Arg Phe
515 520 525

Ser Ile Asn Ile Ser Leu Pro Leu Thr Lys Asp Tyr Gly His Ile Ser
530 535 540

Ser Asn Tyr Ser Phe Ser Asn Ala Asn Thr Gly Thr Ala Thr Ser Ser
545 550 555 560

Val Gly Leu Asn Gly Ser Phe Phe Asn Asp Ala Arg Leu Asn Trp Asn
565 570 575

Ile Gln Gln Asn Arg Thr Thr Arg Asn Asn Gly Tyr Thr Asp Asn Thr
580 585 590

Ser Tyr Ile Ala Thr Ser Tyr Ala Ser Pro Tyr Gly Val Phe Thr Gly
595 600 605

Ser Tyr Ser Gly Ser Asn Lys Tyr Ser Ser Gln Phe Tyr Ser Ala Ser
610 615 620

Gly Gly Ile Val Leu His Ser Asp Gly Val Ala Phe Thr Gln Lys Ala
625 630 635 640

Gly Asp Thr Ser Ala Leu Val Arg Ile Asp Asn Ile Ser Asp Ile Lys
645 650 655

Ile Gly Asn Thr Pro Gly Val Tyr Thr Gly Tyr Asn Gly Phe Ala Leu
660 665 670

Ile Pro His Leu Gln Pro Phe Lys Lys Asn Thr Ile Leu Ile Asn Asp
675 680 685

Lys Gly Ile Pro Asp Gly Ile Thr Leu Ala Asn Ile Lys Lys Gln Val
690 695 700

Ile Pro Ser Arg Gly Ala Ile Val Lys Val Lys Phe Asp Ala Lys Lys
705 710 715 720

Gly Asn Asp Ile Leu Phe Lys Leu Thr Thr Lys Asp Gly Lys Thr Pro
725 730 735

Pro Leu Gly Ala Ile Ala His Glu Lys Asn Gly Lys Gln Ile Asn Thr
740 745 750

Gly Ile Val Asp Asp Asp Gly Met Leu Tyr Met Ser Gly Leu Ser Gly
755 760 765

Thr Gly Ile Ile Asn Val Thr Trp Asn Gly Lys Val Cys Ser Phe Pro
770 775 780

Phe Ser Glu Lys Asp Ile Ser Ser Lys Gln Leu Ser Val Val Asn Lys
785 790 795 800

Gln Cys

(2) INFORMATION FOR SEQ ID NO:9:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 136 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Arg Thr Glu Ile Ala Thr Lys Asn Phe Pro Val Ser Thr Thr Ile Ser
1 5 10 15

Lys Ser Phe Phe Ala Pro Glu Pro Arg Ile Gln Pro Ser Phe Gly Glu
20 25 30

Asn Val Gly Lys Glu Gly Ala Leu Leu Phe Ser Val Asn Leu Thr Val
35 40 45

Pro Glu Asn Val Ser Gln Val Thr Val Tyr Pro Val Tyr Asp Glu Asp
50 55 60

Tyr Gly Leu Gly Arg Leu Val Asn Thr Ala Asp Ala Ser Gln Ser Ile
65 70 75 80

Ile Tyr Gln Ile Val Asp Glu Lys Gly Lys Lys Met Leu Lys Asp His
85 90 95

Gly Ala Glu Val Thr Pro Asn Gln Gln Ile Thr Phe Lys Ala Leu Asn
100 105 110

Tyr Thr Ser Gly Glu Lys Lys Ile Ser Pro Gly Ile Tyr Asn Asp Gln
115 120 125

Val Met Val Gly Tyr Tyr Val Asn
130 135

(2) INFORMATION FOR SEQ ID NO:10:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 146 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(iii) HYPOTHETICAL: NO

(iv) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Asn Trp Gln Tyr Lys Ser Leu Asp Val Asn Val Asn Ile Glu Gln
1 5 10 15

Asn Phe Ile Pro Asp Ile Asp Ser Ala Val Arg Ile Ile Pro Val Asn
20 25 30

Tyr Asp Ser Asp Pro Lys Leu Asp Ser Gln Leu Tyr Thr Val Glu Met
35 40 45

Thr Ile Pro Ala Gly Val Ser Ala Val Lys Ile Ala Pro Thr Asp Ser
50 55 60

Leu Thr Ser Ser Gly Gln Gln Ile Gly Lys Leu Val Asn Val Asn Asn
65 70 75 80

Pro Asp Gln Asn Met Asn Tyr Tyr Ile Arg Lys Asp Ser Gly Ala Gly
85 90 95

Asn Phe Met Ala Gly Gln Lys Gly Ser Phe Pro Val Lys Glu Asn Thr
100 105 110

Ser Tyr Thr Phe Ser Ala Ile Tyr Thr Gly Gly Glu Tyr Pro Asn Ser
115 120 125

Gly Tyr Ser Ser Gly Thr Tyr Ala Gly Asn Leu Thr Val Ser Phe Tyr
130 135 140

Ser Asn
145